

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL.

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

**STAFF USE ONLY**

	Type of Search	Vendors and cost where applicable
Searcher: <u>P. Schweitzer</u>	NA Sequence (#) <u>2</u>	STN _____
Searcher Phone #: <u>272-3526</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Ransom EOI A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>4/2</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>14</u>	Fulltext _____	Sequence Systems <u>Compukey</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>6</u>	Other _____	Other (specify) _____

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:45:11 ; Search time 38.4872 Seconds  
(without alignments)  
273.963 Million cell updates/sec

Title: US-09-520-538-16

Perfect score: 19  
Sequence: 1 ccgcgatgcatcatttg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCUTS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	78.9	275	4	US-09-313-294A-2133
C 2	14.8	77.9	853	4	US-08-858-207A-112
C 3	14.8	77.9	1920	4	US-09-543-681A-1976
C 4	14.8	77.9	8898	4	US-08-961-527-69
C 5	14.4	75.8	21	4	US-09-501-612A-24
C 6	14.4	75.8	519	4	US-08-936-165A-50
C 7	14.4	75.8	852	4	US-08-956-171E-763
C 8	14.4	75.8	1893	4	US-08-956-171E-155
C 9	14.4	75.8	3294	3	US-08-409-995-1
C 10	14.4	75.8	3294	3	US-08-685-467-1
C 11	14.4	75.8	3294	3	US-08-913-942-1
C 12	14.4	75.8	3294	3	US-09-268-347-43
C 13	14.4	75.8	3300	4	US-09-268-347-31
C 14	14.4	75.8	3494	4	US-09-501-612A-1
C 15	14.4	75.8	1230025	4	US-09-198-452A-1
C 16	14.2	74.7	766	3	US-08-818-112-1
C 17	14.2	74.7	766	4	US-08-818-112-1
C 18	14.2	74.7	766	4	US-09-056-556-1
C 19	14.2	74.7	766	4	US-09-072-596-1
C 20	14.2	74.7	766	4	US-09-072-596-1
C 21	14.2	74.7	903	4	US-09-252-991A-7376
C 22	14.2	74.7	926	4	US-09-540-236-1131
C 23	14.2	74.7	1461	4	US-09-335-586-2
C 24	14.2	74.7	1749	4	US-09-721-870-178
C 25	14.2	74.7	2355	4	US-09-543-681A-3270
C 26	14.2	74.7	7876	1	US-08-225-480-1
C 27	14.2	74.7	7876	4	US-09-118-445-1

C 28	14.2	74.7	7876	5	PCT-US93-08115-1	Sequence 1, Appli
C 29	14.2	74.7	33778	4	US-09-536-002-19	Sequence 19, Appli
C 30	14.2	74.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 31	14.2	74.7	4403765	3	US-09-103-840A-2	Sequence 1, Appli
C 32	14.2	74.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 33	14.2	74.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 34	14	73.7	2742	4	US-09-107-532A-613	Sequence 613, Appli
C 35	14	73.7	40090	4	US-09-820-004-3	Sequence 3, Appli
C 36	13.8	72.6	141	4	US-09-445-388A-9	Sequence 9, Appli
C 37	13.8	72.6	441	4	US-09-621-976-18101	Sequence 18101, A
C 38	13.8	72.6	459	4	US-09-621-976-18106	Sequence 18106, A
C 39	13.8	72.6	916	4	US-09-247-155-134	Sequence 134, App
C 40	13.8	72.6	1086	4	US-09-134-000C-1031	Sequence 1031, Ap
C 41	13.8	72.6	1220	3	US-09-116-032-2	Sequence 2, Appli
C 42	13.8	72.6	1227	6	5474928-1	Sequence 134, App
C 43	13.8	72.6	1359	4	US-09-489-039A-49	Sequence 49, Appli
C 44	13.8	72.6	1381	4	US-08-936-165A-225	Sequence 225, App
C 45	13.8	72.6	1536	3	US-09-352-990-17	Sequence 17, Appli

## ALIGNMENTS

RESULT 1  
US-09-313-294A-2133/c  
; Sequence 2133, Application US/09313294A

; Patent No. 6476212  
; GENERAL INFORMATION:

; APPLICANT: Lalguadi, Raghunath V.  
; APPLICANT: Ito, Laura Y.

; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A

; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600

; SOFTWARE: PERL Program  
; SEQ ID NO 2133

; LENGTH: 275  
; TYPE: DNA

; ORGANISM: Zea mays  
; FEATURE:

; NAME/KEY: misc feature  
; OTHER INFORMATION: Inocyte ID No. 6476212 700552137H1

; US-09-313-294A-2133

Query Match 78.9%; Score 15; DB 4; Length 275;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCATTGATCATTTG 18  
Db 138 TCATTGATCATTTG 124

RESULT 2  
US-08-858-207A-112/c  
; Sequence 112, Application US/08858207A

; Patent No. 6348328  
; GENERAL INFORMATION:

; APPLICANT: Black, Michael  
; APPLICANT: Hodgson, John

; APPLICANT: Knowles, David  
; APPLICANT: Nicholas, Richard

; APPLICANT: Stodola, Robert  
; TITLE OF INVENTION: No. 6348328el Compounds

; NUMBER OF SEQUENCES: 552  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road

; CITY: King of Prussia  
; STATE: PA

; COUNTRY: USA

ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmli, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 853 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-858-207A-112

Query Match 77.9%; Score 14.8; DB 4; Length 853;  
Best Local Similarity 88.9%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTCGATTGATCATTTG 18  
Db 361 CCGTCGATTGATCATTTG 344

RESULT 3  
US-09-543-681A-1976/c  
Sequence 1976, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709,1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 1976  
LENGTH: 1920  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-1976

Query Match 77.9%; Score 14.8; DB 4; Length 1920;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTCGATTGATCATTTG 18  
Db 993 CCGTCGATTGATCATTTG 976

RESULT 4  
US-08-961-527-69  
Sequence 69, Application US/08961527  
Patent No. 6420135  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 391  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,527  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-961-527-69

Query Match 77.9%; Score 14.8; DB 4; Length 8898;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTCGATTGATCATTTG 18  
Db 5002 CCGTCGATTGATCATTTG 5019

RESULT 5  
US-09-501-612A-24  
Sequence 24, Application US/09501612A  
Patent No. 6544765  
GENERAL INFORMATION:  
APPLICANT: Hjort, Carsten M.  
TITLE OF INVENTION: Oxalacetate Hydrolyase Deficient Fungal Host Cells  
FILE REFERENCE: 5789,200-US  
CURRENT APPLICATION NUMBER: US/09/501,612A  
CURRENT FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 24  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-501-612A-24

Query Match 75.8%; Score 14.4; DB 4; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGTCGATTGATCATTT 17  
Db 6 CCGTCGATTGATCATTT 21

RESULT 6  
US-08-936-165A-50/c  
Sequence 50, Application US/08936165A  
Patent No. 6348582  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Burnham, Martin  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Lometto, Michael  
APPLICANT: Nicholas, Richard  
APPLICANT: Pratt, Julie  
APPLICANT: Reichard, Richard  
APPLICANT: Rosenberg, Martin  
APPLICANT: Ward, Judith  
TITLE OF INVENTION: No. 6348582e1 Prokaryotic Polynucleotides,  
TITLE OF INVENTION: Polypeptides and Their Uses  
NUMBER OF SEQUENCES: 534  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/936,165A  
FILING DATE: 24-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,032  
FILING DATE: 24-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmè, Edward R.  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50549  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-936-165A-50  
Query Match 75.8%; Score 14.4; DB 4; Length 519;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGATGATCATTT 17  
|||  
DB 157 COTCATGATCATTT 142

RESULT 7  
US-08-956-171E-763  
Sequence 763, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon

Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
MEDM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark V. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 763:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 852 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 763:  
US-08-956-171E-763  
Query Match 75.8%; Score 14.4; DB 4; Length 852;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCGATGATCATTTG 18  
|||  
DB 23 GTCGATGATCATTTG 38

RESULT 8  
US-08-956-171E-155  
Sequence 155, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gill H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

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; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 155:
US-08-956-171E-155

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Query Match          75.8%; Score 14.4; DB 4; Length 1893;
Best Local Similarity 93.8%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 CGTCATGATCATTT 17
Db      1578 CGTCATGATCATTT 1593

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RESULT 9
US-08-409-995-1/c
; Sequence 1, Application US/08409995
; Patent No. 5646259
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen I.
; APPLICANT: St. Gene III, Joseph W.
; TITLE OF INVENTION: Haemophilus Adhesion Proteins
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,995
; FILING DATE: 24-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61053/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3294 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
US-08-409-995-1

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Query Match          75.8%; Score 14.4; DB 1; Length 3294;
Best Local Similarity 93.8%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      4 TCGATTGATCATTTGG 19
Db      2905 TCGATTGATCATTTGG 2890

```

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RESULT 10
US-08-685-467-1/c
; Sequence 1, Application US/08685467
; Patent No. 6060059
; GENERAL INFORMATION:
; APPLICANT: St. Gene III, Joseph W.
; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,467
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,995
; FILING DATE: 24-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-685-467-1

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Query Match          75.8%; Score 14.4; DB 3; Length 3294;
Best Local Similarity 93.8%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4 TCGATTGATCATTTGG 19
Db      2905 TCGATTGATCATTTGG 2890

```

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RESULT 11
US-08-913-942-1/c
; Sequence 1, Application US/08913942
; Patent No. 6200578
; GENERAL INFORMATION:

```

APPLICANT: St. Geme, Joseph  
APPLICANT: Barenkamp, Stephen J.  
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Flehr Hohbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/913,942  
APPLICATION NUMBER: US/08/913,942  
FILING DATE: 29-DEC-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/409,995  
FILING DATE: 24-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/4031  
FILING DATE: 22-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Vance, Dolly A.  
REGISTRATION NUMBER: 39,054  
REFERENCE/DOCKET NUMBER: A-61053-1-RTT/RMS/DAV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3294 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-913-942-1

Query Match 75.8%; Score 14.4; DB 3; Length 3294;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCGATTGATCATTTGG 19  
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DB 2905 TTGATTGATCATTTGG 2890

RESULT 12  
US-09-268-347-43/C  
Sequence 43, Application US/09268347  
Patent No. 6335182  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS  
FILE REFERENCE: 1038-860  
CURRENT APPLICATION NUMBER: US/09/268,347  
CURRENT FILING DATE: 1999-03-16  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4394  
LENGTH: 3294  
TYPE: DNA  
ORGANISM: Haemophilus influenzae  
US-09-268-347-43

Query Match 75.8%; Score 14.4; DB 4; Length 3294;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 2905 TTGATTGATCATTTGG 2890

RESULT 13  
US-09-268-347-31/C  
Sequence 31, Application US/09268347  
Patent No. 6335182  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS  
FILE REFERENCE: 1038-860  
CURRENT APPLICATION NUMBER: US/09/268,347  
CURRENT FILING DATE: 1999-03-16  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 31  
LENGTH: 3300  
TYPE: DNA  
ORGANISM: Haemophilus influenzae  
US-09-268-347-31

Query Match 75.8%; Score 14.4; DB 4; Length 3300;  
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 2893 TTGATTGATCATTTGG 2878

RESULT 14  
US-09-501-612A-1  
Sequence 1, Application US/09501612A  
Patent No. 6544765  
GENERAL INFORMATION:  
APPLICANT: Hjort, Carsten M.  
TITLE OF INVENTION: Oxalacetate Hydrolase Deficient Fungal Host Cells  
FILE REFERENCE: 5789.200-US  
CURRENT APPLICATION NUMBER: US/09/501,612A  
CURRENT FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 3494  
TYPE: DNA  
ORGANISM: Aspergillus niger  
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NAME/KEY: Initon  
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NAME/KEY: CDS  
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US-09-501-612A-1

Query Match 75.8%; Score 14.4; DB 4; Length 3494;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;

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Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0,
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Db 712 CGTCGATTGATCATTT 727

RESULT 15
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
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Search completed: April 1, 2004, 13:06:28  
 Job time : 44.4872 secs

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Query Match 75.8%; Score 14.4; DB 4; Length 1230025;  
 Best Local Similarity 93.8%; Pred. No. 2,4e+02;  
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QY 4 TCGATTGATCATTTGG 19  
 Db 98696 TTGATTGATCATTTGG 98711



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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:48:52 ; Search time 139.333 Seconds  
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Title: US-09-520-538-16

Perfect score: 19

Sequence: 1 ccgcgcattgattgg 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2465228 seqs, 1869859620 residues

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Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.\*  
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18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	19	9	US-09-520-538-16	Sequence 16, Appl
2	15.8	83.2	1332	US-08-910-386A-12	Sequence 12, Appl
3	15.8	83.2	1873	US-10-369-493-26085	Sequence 26085, A
4	15.4	81.1	143068	US-09-967-768A-316	Sequence 316, App
5	15.4	81.1	1601042	US-10-027-632-59064	Sequence 59064, A
6	15.4	235	12	US-10-424-599-131971	Sequence 131971, A
7	15.4	78.9	5563	US-10-398-221-3814	Sequence 3814, Ap
8	15.4	78.9	713059	US-10-027-632-174581	Sequence 174581, A
9	15.4	78.9	2340917	US-10-027-632-174763	Sequence 174763, A
10	14.8	77.9	381	US-10-424-599-11595	Sequence 11595, A
11	14.8	77.9	396	US-09-864-408A-7871	Sequence 7871, Ap
12	14.8	77.9	648	US-10-027-632-54944	Sequence 54944, A
13	14.8	77.9	648	US-10-027-632-313387	Sequence 313387, A
14	14.8	77.9	669	US-10-027-632-689	Sequence 689, App
15	14.8	77.9	1032	US-10-369-493-32752	Sequence 32752, A

16	14.8	77.9	1139	12	US-10-425-114-36032	Sequence 36032, A
17	14.8	77.9	1146	10 <td>US-09-738-626-3061</td> <td>Sequence 3061, Ap</td>	US-09-738-626-3061	Sequence 3061, Ap
18	14.8	77.9	1170	9 <td>US-09-746-660A-79</td> <td>Sequence 79, Appl</td>	US-09-746-660A-79	Sequence 79, Appl
19	14.8	77.9	1233	15 <td>US-10-369-493-36091</td> <td>Sequence 36091, A</td>	US-10-369-493-36091	Sequence 36091, A
20	14.8	77.9	1875	12 <td>US-10-282-122A-32282</td> <td>Sequence 32282, A</td>	US-10-282-122A-32282	Sequence 32282, A
21	14.8	77.9	2298	15 <td>US-10-398-221-1889</td> <td>Sequence 1889, Ap</td>	US-10-398-221-1889	Sequence 1889, Ap
22	14.8	77.9	2628	9 <td>US-09-919-831-1</td> <td>Sequence 1, Appl1</td>	US-09-919-831-1	Sequence 1, Appl1
23	14.8	77.9	5093	10 <td>US-09-949-029-110</td> <td>Sequence 109, App</td>	US-09-949-029-110	Sequence 109, App
24	14.8	77.9	6751	10 <td>US-09-949-029-109</td> <td>Sequence 69, Appl</td>	US-09-949-029-109	Sequence 69, Appl
25	14.8	77.9	8898	12 <td>US-10-158-844-69</td> <td>Sequence 69, Appl</td>	US-10-158-844-69	Sequence 69, Appl
26	14.8	77.9	3309400	9 <td>US-09-738-626-1</td> <td>Sequence 24, Appl1</td>	US-09-738-626-1	Sequence 24, Appl1
27	14.4	75.8	21	14 <td>US-10-336-491-24</td> <td>Sequence 840, App</td>	US-10-336-491-24	Sequence 840, App
28	14.4	75.8	272	12 <td>US-10-085-783A-840</td> <td>Sequence 840, App</td>	US-10-085-783A-840	Sequence 840, App
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30	14.4	75.8	299	9 <td>US-09-910-664-58</td> <td>Sequence 58, Appl</td>	US-09-910-664-58	Sequence 58, Appl
31	14.4	75.8	316	12 <td>US-10-085-783A-55876</td> <td>Sequence 55876, A</td>	US-10-085-783A-55876	Sequence 55876, A
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33	14.4	75.8	456	9 <td>US-09-974-300-4309</td> <td>Sequence 4309, Ap</td>	US-09-974-300-4309	Sequence 4309, Ap
34	14.4	75.8	519	9 <td>US-09-939-980-50</td> <td>Sequence 50, Appl</td>	US-09-939-980-50	Sequence 50, Appl
35	14.4	75.8	582	15 <td>US-10-027-632-190553</td> <td>Sequence 190553, A</td>	US-10-027-632-190553	Sequence 190553, A
36	14.4	75.8	582	15 <td>US-10-027-632-217359</td> <td>Sequence 217359, A</td>	US-10-027-632-217359	Sequence 217359, A
37	14.4	75.8	706	15 <td>US-10-027-632-146373</td> <td>Sequence 146373, A</td>	US-10-027-632-146373	Sequence 146373, A
38	14.4	75.8	795	12 <td>US-10-425-114-20145</td> <td>Sequence 20145, A</td>	US-10-425-114-20145	Sequence 20145, A
39	14.4	75.8	852	8 <td>US-08-781-986A-763</td> <td>Sequence 763, App</td>	US-08-781-986A-763	Sequence 763, App
40	14.4	75.8	852	12 <td>US-10-329-624-763</td> <td>Sequence 763, App</td>	US-10-329-624-763	Sequence 763, App
41	14.4	75.8	942	9 <td>US-09-738-626-320</td> <td>Sequence 320, App</td>	US-09-738-626-320	Sequence 320, App
42	14.4	75.8	1314	9 <td>US-09-815-242-4185</td> <td>Sequence 4185, Ap</td>	US-09-815-242-4185	Sequence 4185, Ap
43	14.4	75.8	1338	9 <td>US-09-815-242-8484</td> <td>Sequence 8484, Ap</td>	US-09-815-242-8484	Sequence 8484, Ap
44	14.4	75.8	1338	12 <td>US-10-282-122A-8166</td> <td>Sequence 8166, Ap</td>	US-10-282-122A-8166	Sequence 8166, Ap
45	14.4	75.8	1824	15 <td>US-10-369-493-32855</td> <td>Sequence 32855, A</td>	US-10-369-493-32855	Sequence 32855, A

## ALIGNMENTS

RESULT 1  
US-09-520-538-16  
Sequence 16, Application US/09520538  
Patent No. US20020168636A1  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
APPLICANT: Wise, Arlene  
TITLE OF INVENTION: Detection Of Phenols Using Engineered Bacteria  
FILE REFERENCE: S-91, 714  
CURRENT APPLICATION NUMBER: US/09/520,538  
CURRENT FILING DATE: 2000-03-08  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Pseudomonas sp. CF600  
US-09-520-538-16

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGATTCATTCATTTGG 19  
DB 1 CCCTGATTCATTCATTTGG 19  
RESULT 2  
US-08-910-386A-12  
Sequence 12, Application US/08910386A  
Publication No. US2002092041A1  
GENERAL INFORMATION:  
APPLICANT: Ronald, Pamela C.  
APPLICANT: Wang, Guo-Liang  
APPLICANT: Song, Wen-Yuang  
APPLICANT: Hulbert, Scot  
APPLICANT: Richter, Todd

TITLE OF INVENTION: Procedures and Materials for Conferring  
TITLE OF INVENTION: Disease Resistance in Plants  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,386A  
FILING DATE: 13-AUG-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-058950US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 12:  
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LENGTH: 1332 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
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ORGANISM: Oryza longistaminata  
STRAIN: IRBB21  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 11  
MAP POSITION: 11q, RG103  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1332 /note="3' flanking sequence of Xa21  
OTHER INFORMATION: gene family member F"  
US-08-910-386A-12  
Query Match 83.2%; Score 15.8; DB 8; Length 1332;  
Best Local Similarity 89.5%; Pred. No. 4.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CCGTCGATTGATTCATTGG 19  
2 CCGTCGATCATCATTTGG 20  
RESULT 3  
US-10-369-493-26085/c  
Sequence 26085, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 26085  
LENGTH: 1873  
TYPE: DNA  
ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-26085  
Query Match 83.2%; Score 15.8; DB 15; Length 1873;  
Best Local Similarity 89.5%; Pred. No. 4.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CCGTCGATTGATTCATTGG 19  
2 CCGTCGATCATCATTTGG 206  
RESULT 4  
US-09-967-768A-316  
Sequence 316, Application US/09967768A  
Patent No. US20020150877A1  
GENERAL INFORMATION:  
APPLICANT: Augustus, Meena  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
TITLE OF INVENTION: Sets  
FILE REFERENCE: 689290-72  
CURRENT APPLICATION NUMBER: US/09/967,768A  
CURRENT FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: US/60/236,109  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US/60/236,034  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US/60/236,111  
PRIOR FILING DATE: 2000-09-28  
NUMBER OF SEQ ID NOS: 325  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 316  
LENGTH: 143068  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-967-768A-316  
Query Match 81.1%; Score 15.4; DB 9; Length 143068;  
Best Local Similarity 94.1%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 GTCGATTGATTCATTGG 19  
21265 GTCGATTGATTCATTGG 21281  
RESULT 5  
US-10-027-632-59064/c  
Sequence 59064, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002

```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 59064
; LENGTH: 1601042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1601042)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-59064

```

```

Query Match      81.1%; Score 15.4; DB 15; Length 1601042;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CCGTGCATTCATTCATTGG 19
Db      687632 CCGCGATTCATTCATTCATTGG 687614

```

```

RESULT 6
US-10-424-599-131971/C
; Sequence 131971, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 131971
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90177C.1
US-10-424-599-131971

```

```

Query Match      78.9%; Score 15; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCGATTGATTCATTGG 18
Db      96 TCGATTGATTCATTGG 82

```

```

RESULT 7
US-10-398-221-3814
; Sequence 3814, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KONST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3814
; LENGTH: 5563

```

```

; TYPE: DNA
; ORGANISM: Listeria monocytogenes 4b
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3814

```

```

Query Match      78.9%; Score 15; DB 15; Length 5563;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCGATTGATTCATTGG 18
Db      1748 TCGATTGATTCATTGG 1762

```

```

RESULT 8
US-10-027-632-174581
; Sequence 174581, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174581
; LENGTH: 713059
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(713059)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174581

```

```

Query Match      78.9%; Score 15; DB 15; Length 713059;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CCGTGCATTCATTCATTGG 19
Db      667865 BCGTCATTCATTCATTGG 667883

```

```

RESULT 9
US-10-027-632-174763
; Sequence 174763, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

```

```

; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763
```

```

Query Match      78.9%; Score 15; DB 15; Length 2940917;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 TCGATTGATCATTTG 18
DB      780290 TCGATTGATCATTTG 780304
```

```

RESULT 10
US-10-424-599-11595
; Sequence 11595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 11595
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110479C.1
US-10-424-599-11595
```

```

Query Match      77.9%; Score 14.8; DB 12; Length 381;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CCGTGATTTGATTTG 18
DB      93 CCGTGATTTGAGCAGTTG 110
```

```

RESULT 11
US-09-864-408A-7871/c
; Sequence 7871, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7871
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (360)...(360)
; OTHER INFORMATION: wherein n may be a, c, g or t
US-09-864-408A-7871
```

```

Query Match      77.9%; Score 14.8; DB 11; Length 396;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CCGTGATTTGATTTG 18
DB      41 CCGTGATTTGATTTG 24
```

```

RESULT 12
US-10-027-632-54944
; Sequence 54944, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 54944
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54944
```

```

Query Match      77.9%; Score 14.8; DB 15; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CGTGATTTGATTTG 19
DB      424 CGTGATTTGATTTG 441
```

```

RESULT 13
US-10-027-632-313387
; Sequence 313387, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 313387
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-313387

Query Match      77.9%; Score 14.8; DB 15; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CCTGCATTGATCATTTGG 19
DB      424  CCTGCATTGATCATTTGG 441

RESULT 14
US-10-027-632-689
; Sequence 689, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 60/146,002
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 313387
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-313387

Query Match      77.9%; Score 14.8; DB 15; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CCTGCATTGATCATTTGG 19
DB      424  CCTGCATTGATCATTTGG 441

```

```

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 689
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-689

Query Match      77.9%; Score 14.8; DB 15; Length 669;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CCTGCATTGATCATTTGG 19
DB      465  CCTGCATTGATCATTTGG 482

RESULT 15
US-10-369-493-32752
; Sequence 32752, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory T.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32752
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Chloroflexus aurantiacus
US-10-369-493-32752

Query Match      77.9%; Score 14.8; DB 15; Length 1032;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CCGGCGATTGATCATTTGG 18
DB      922  CCGGCGATTGATCATTTGG 939

Search completed: April 1, 2004, 13:13:33
Job time : 145.333 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:45:11 ; Search time 40.5128 Seconds  
(without alignments)  
273.963 Million cell updates/sec

Title: US-09-520-538-17

Perfect score: 20

Sequence: 1 tgcacatcatgacgacac 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/ECTUS.COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backfillseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.4	82.0	1770	1 US-08-241-943-25	Sequence 25, Appl
C 2	16.4	82.0	1770	4 US-09-635-132-2	Sequence 2, Appl1
C 3	16.4	82.0	2019	1 US-08-254-357-3	Sequence 3, Appl1
C 4	16.4	82.0	4983	1 US-08-472-358-1	Sequence 1, Appl1
C 5	16.4	82.0	4983	5 PCT-US92-05786A-1	Sequence 1, Appl1
C 6	16.4	82.0	4984	1 US-08-687-806-1	Sequence 1, Appl1
C 7	16.4	82.0	4984	4 US-09-635-132-1	Sequence 103, App
C 8	15.8	79.0	483	4 US-09-252-991A-103	Sequence 99, Appl
C 9	15.8	79.0	993	4 US-09-252-991A-99	Sequence 90, Appl
C 10	15.8	79.0	1065	4 US-09-252-991A-90	Sequence 84, Appl
C 11	15.8	79.0	2934	4 US-09-453-702B-161	Sequence 161, App
C 12	15.8	79.0	2936	4 US-08-403-545-1	Sequence 1, Appl1
C 13	15.8	79.0	6122	3 US-08-404-381-1	Sequence 1, Appl1
C 14	15.8	79.0	582	4 US-09-134-000C-2052	Sequence 2052, Ap
C 15	15.2	76.0	695	3 US-08-998-416-964	Sequence 964, Appl
C 16	15.2	76.0	2260	4 US-09-221-017B-33	Sequence 33, Appl
C 17	15.2	76.0	262	4 US-09-313-294A-2338	Sequence 2338, Ap
C 18	14.8	74.0	1212	4 US-09-540-236-556	Sequence 556, App
C 19	14.8	74.0	1212	4 US-09-543-681A-1205	Sequence 1205, Ap
C 20	14.8	74.0	1680	4 US-09-489-039A-5245	Sequence 5245, Ap
C 21	14.8	74.0	4605	4 US-09-221-017B-128	Sequence 128, App
C 22	14.8	74.0	24535	6 5428147-1	Patent No. 5428147
C 23	14.8	74.0	45613	4 US-09-596-002-22	Sequence 22, Appl
C 24	14.8	74.0	1664976	4 US-08-916-421B-1	Sequence 1, Appl1
C 25	14.8	74.0	1830121	4 US-09-557-884-1	Sequence 1, Appl1
C 26	14.8	74.0	1830121	4 US-09-643-990A-1	Sequence 1, Appl1
C 27	14.8	74.0	1830121	4 US-09-643-990A-1	Sequence 1, Appl1

C 28	14.4	72.0	615	3 US-08-549-515-3	Sequence 3, Appl1
C 29	14.4	72.0	1284	3 US-08-989-510A-15	Sequence 15, Appl
C 30	14.4	72.0	1284	3 US-09-182-816-15	Sequence 15, Appl
C 31	14.4	72.0	1284	3 US-09-471-528-15	Sequence 15, Appl
C 32	14.4	72.0	1284	3 US-09-471-528-15	Sequence 35, Appl
C 33	14.4	72.0	1284	3 US-09-634-530-15	Sequence 35, Appl
C 34	14.4	72.0	1284	3 US-09-634-530-15	Sequence 32, Appl
C 35	14.4	72.0	1326	3 US-09-471-528-12	Sequence 32, Appl
C 36	14.4	72.0	1326	3 US-09-471-528-14	Sequence 32, Appl
C 37	14.4	72.0	1326	3 US-09-634-530-32	Sequence 32, Appl
C 38	14.4	72.0	1326	3 US-08-989-510A-10	Sequence 10, Appl
C 39	14.4	72.0	1392	3 US-08-989-510A-11	Sequence 11, Appl
C 40	14.4	72.0	1392	3 US-09-182-816-10	Sequence 10, Appl
C 41	14.4	72.0	1392	3 US-09-182-816-12	Sequence 12, Appl
C 42	14.4	72.0	1392	3 US-09-471-528-10	Sequence 10, Appl
C 43	14.4	72.0	1392	3 US-09-471-528-12	Sequence 12, Appl
C 44	14.4	72.0	1392	3 US-09-634-530-10	Sequence 10, Appl
C 45	14.4	72.0	1392	3 US-09-634-530-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-08-241-943-25/C  
Sequence 25, Application US/08241943  
Patent No. 5602321  
GENERAL INFORMATION:  
APPLICANT: John, Maliyakal E.  
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Nicholas J. Seay, Charles & Brady  
STREET: First Wisconsin Plaza, One South  
STREET: Pinckney St.  
STREET: P.O. Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,943  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: us/07/980,521  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9076-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-2484  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ. ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1770 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: NO  
PUBLICATION INFORMATION:  
AUTHORS: PEOPLES  
JOURNAL: SINSKEY  
AUTHORS: J. Biol. Chem.  
VOLUME: 264

PAGES: 15298-15303  
DATE: 1989  
US-08-241-943-25

Query Match 82.0%; Score 16.4; DB 1; Length 1770;  
Best Local Similarity 94.4%; Pred. No. 20;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 563 TCCATCATGTGGCGACG 546

RESULT 2  
US-09-635-132-2/c  
Sequence 2, Application US/09635132  
Patent No. 6620601  
GENERAL INFORMATION:  
APPLICANT: YAMAGUCHI, ISAMU  
APPLICANT: NAKASHITA, HIDEO  
APPLICANT: YOSHIOKA, KEIKO  
APPLICANT: DOI, YOSHIMARU  
TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED  
TITLE OF INVENTION: PLANTS AND PROCESSES FOR PREPARATION OF POLYESTERS  
FILE REFERENCE: 081356/0148  
CURRENT APPLICATION NUMBER: US/09/635,132  
CURRENT FILING DATE: 2000-08-09  
PRIORITY APPLICATION NUMBER: JP 11-225832  
PRIORITY FILING DATE: 1999-08-09  
PRIORITY APPLICATION NUMBER: JP 11-225839  
PRIORITY FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1770  
TYPE: DNA  
ORGANISM: Ralstonia eutropha  
US-09-635-132-2

Query Match 82.0%; Score 16.4; DB 4; Length 1770;  
Best Local Similarity 94.4%; Pred. No. 20;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 563 TCCATCATGTGGCGACG 546

RESULT 3  
US-08-254-357-3/c  
Sequence 3, Application US/08254357  
Patent No. 5610041  
GENERAL INFORMATION:  
APPLICANT: Christopher R. Somerville,  
APPLICANT: Christiane Nawrath,  
APPLICANT: Yves Poirier  
TITLE OF INVENTION: Processes For Producing  
TITLE OF INVENTION: Polyhydroxybutyrate and Related  
TITLE OF INVENTION: Polyhydroxyalkanoates in the  
TITLE OF INVENTION: Plastics of Higher Plants  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 5.25 inch, 360 kb  
MEDIUM TYPE: storage  
COMPUTER: Acer  
OPERATING SYSTEM: MS-DOS (version 3.3)

SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/254,357  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/108,193 and 07/732,243  
FILING DATE: August 17, 1993 and July 19, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2019 Base Pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
ORGANISM: Alcaligenes eutrophus  
IMMEDIATE SOURCE:  
LIBRARY: Genomic

US-08-254-357-3

Query Match 82.0%; Score 16.4; DB 1; Length 2019;  
Best Local Similarity 94.4%; Pred. No. 20;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 812 TCCATCATGTGGCGACG 795

RESULT 4  
US-08-472-358-1/c  
Sequence 1, Application US/08472358  
Patent No. 5650555  
GENERAL INFORMATION:  
APPLICANT: Chris Somerville, Yves Poirier,  
APPLICANT: Douglas Dennis  
TITLE OF INVENTION: Transgenic Plant Materials  
TITLE OF INVENTION: Producing Polyhydroxyalkanoates  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 5.25 inch, 360 kb  
MEDIUM TYPE: storage  
COMPUTER: IBM AT  
OPERATING SYSTEM: MS-DOS (version 3.3)  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,358  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/732,243  
FILING DATE: July 19, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4983 Base Pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
ORGANISM: Alcaligenes eutrophus  
IMMEDIATE SOURCE:  
LIBRARY: Genomic  
US-08-472-358-1

Query Match 82.0%; Score 16.4; DB 1; Length 4983;  
Best Local Similarity 94.4%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATCATATTGGCGACG 20  
DB 1407 TCATCATATTGGCGACG 1390

## RESULT 5

PCT-US92-05786A-1/c  
Sequence 1, Application PC/US9205786A

GENERAL INFORMATION:  
APPLICANT: Michigan State University  
TITLE OF INVENTION: Transgenic Plant Materials  
TITLE OF INVENTION: Producing Polyhydroxyalkanoates  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: T. David Reed,  
ADDRESS: The Procter & Gamble Company  
ADDRESSEE: Patent Division - International  
STREET: 5299 Spring Grove Avenue  
CITY: Cincinnati  
STATE: Ohio  
COUNTRY: USA  
ZIP: 45217

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 5.25 inch, 360 kb  
MEDIUM TYPE: storage  
COMPUTER: IBM AT

OPERATING SYSTEM: MS-DOS (version 3.3)  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05786A

FILING DATE: 19920713  
FILING DATE: priority under the Paris Convention  
FILING DATE: to the prior U.S. filing.  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/732,243  
FILING DATE: 19 July 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: T. David Reed

REGISTRATION NUMBER: 32,931

REFERENCE/DOCKET NUMBER: 4638#

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (513) 627-7025  
TELEFAX: (513) 627-6333

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4983 Base Pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double

TOPOLOGY: Linear  
MOLECULE TYPE:  
DESCRIPTION: Genomic DNA  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
ORGANISM: Alcaligenes eutrophus  
IMMEDIATE SOURCE:  
LIBRARY: Genomic  
PCT-US92-05786A-1

Query Match 82.0%; Score 16.4; DB 5; Length 4983;  
Best Local Similarity 94.4%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATCATATTGGCGACG 20  
DB 1407 TCATCATATTGGCGACG 1390

## RESULT 6

US-08-687-806-1/c  
Sequence 1, Application US/08687806  
Patent No. 5811272

GENERAL INFORMATION:  
APPLICANT: Snell, Kristi D.  
APPLICANT: Hogan, Scott A.  
APPLICANT: Sim, Sang Jun  
APPLICANT: Sinskey, Anthony J.  
APPLICANT: Rha, Chokyun  
TITLE OF INVENTION: Method for Controlling Molecular Weight of  
TITLE OF INVENTION: Polyhydroxyalkanoates  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,806

FILING DATE: 11-Jul-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: mt 6867  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-873-8794

TELEFAX: 404-873-8795

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 4984 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-687-806-1

Query Match 82.0%; Score 16.4; DB 1; Length 4984;  
Best Local Similarity 94.4%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATCATATTGGCGACG 20  
DB 1404 TCATCATATTGGCGACG 1387



RESULT 7  
US-09-635-132-1/c  
; Sequence 1, Application US/09635132  
; Patent No. 6620601  
; GENERAL INFORMATION:  
; APPLICANT: YAMAGUCHI, ISAMU  
; APPLICANT: NAKASHITA, HIDEO  
; APPLICANT: YOSHIOKA, KEIKO  
; APPLICANT: DOI, YOSHIMARU  
; TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED  
; TITLE OF INVENTION: PLANTS AND PROCESSES FOR PREPARATION OF POLYESTERS  
; FILE REFERENCE: 081356/0148  
; CURRENT APPLICATION NUMBER: US/09/635,132  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: JP 11-225832  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: JP 11-225839  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patentia Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4984  
; TYPE: DNA  
; ORGANISM: Ralstonia eutrophia  
US-09-635-132-1

Query Match 82.0%; Score 16.4; DB 4; Length 4984;  
Best Local Similarity 94.4%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTCATCATATTGGCGACG 20  
DB 1404 TTCATCATATTGGCGACG 1387

RESULT 8  
US-09-252-991A-103  
; Sequence 103, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 103  
; LENGTH: 483  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-103

Query Match 79.0%; Score 15.8; DB 4; Length 483;  
Best Local Similarity 89.5%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATCATATTGGCGACG 20  
DB 165 GTCCATCATATTGGCGACG 183

RESULT 9  
US-09-252-991A-99  
; Sequence 99, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 99  
; LENGTH: 993  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-99

Query Match 79.0%; Score 15.8; DB 4; Length 993;  
Best Local Similarity 89.5%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATCATATTGGCGACG 20  
DB 574 GTCCATCATATTGGCGACG 592

RESULT 10  
US-09-252-991A-90/c  
; Sequence 90, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 90  
; LENGTH: 1065  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-90

Query Match 79.0%; Score 15.8; DB 4; Length 1065;  
Best Local Similarity 89.5%; Pred. No. 38;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATCATATTGGCGACG 20  
DB 957 GTCCATCATATTGGCGACG 939

RESULT 11  
US-09-252-991A-84/c  
; Sequence 84, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 84

LENGTH: 2934  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-84

Query Match 79.0%; Score 15.8; DB 4; Length 2934;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCATCATATTGGCGACG 20  
|||||  
Db 1180 GTTCATCATCTTGGCGACG 1162

RESULT 12  
US-09-453-702B-161/C  
Sequence 161, Application US/09453702B  
Patent No. 6365723  
GENERAL INFORMATION:  
APPLICANT: Blattner, Frederick R.  
Burland, Valerie  
Perna, Nicole T.  
Plunkett, Guy  
Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453, 702B  
FILING DATE: 03-Dec-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/110,955  
FILING DATE: 04-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ ID NO: 161:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2936  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 161:

US-09-453-702B-161

Query Match 79.0%; Score 15.8; DB 4; Length 2936;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCATCATATTGGCGAC 19  
|||||  
Db 2857 TGTCATCATCTTGGCGAC 2839

RESULT 13  
US-08-403-545-1/C

Sequence 1, Application US/08403545  
Patent No. 5656483  
GENERAL INFORMATION:  
APPLICANT: Sokatch, John R.  
APPLICANT: Sykes, Pamela Joy  
APPLICANT: Madhusudan, K.T.  
TITLE OF INVENTION: Genes Encoding Operon and Promoter for  
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putida  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carolyn D. Moon  
ADDRESSEE: Dunlap, Codding, Peterson and Lee  
STREET: 9400 N. Broadway, Suite 420  
CITY: Oklahoma City  
STATE: Oklahoma  
COUNTRY: USA  
ZIP: 73114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 5.25 inch, 360 Kb Storage  
COMPUTER: IBM AT  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Professional Write 2.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,545  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 7/603/781  
APPLICATION NUMBER: 07/172,148  
FILING DATE: 23-003-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Carolyn D. Moon  
REGISTRATION NUMBER: 33,022  
REFERENCE/DOCKET NUMBER: 5820.101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: Attorney, (405) 478-5344  
TELEFAX: Attorney, (405) 478-5349  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6122 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Double stranded  
TOPOLOGY: Circular  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: Seq ID No. 5656483 is genomic DNA from P. putida  
DESCRIPTION: strain Pg2 which contains the control region regulating  
DESCRIPTION: expression of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No. 5656483 applicable  
ORIGINAL SOURCE:  
ORGANISM: Pseudomonas putida  
STRAIN: Pg2  
INDIVIDUAL ISOLATE: No. 5656483 applicable  
DEVELOPMENTAL STAGE: No. 5656483 applicable  
HAPLOTYPE: No. 5656483 applicable  
TISSUE TYPE: No. 5656483 applicable  
CELL TYPE: Gram negative, aerobic bacilli  
CELL LINE: No. 5656483 applicable  
ORGANELLER: No. 5656483 applicable  
IMMEDIATE SOURCE:  
LIBRARY: Genomic DNA from Pseudomonas putida  
CLONE: pJRS54  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION: 35 Minutes  
UNITS:  
FEATURE:  
NAME/KEY: Promoter plus leader  
LOCATION: 1-792

IDENTIFICATION METHOD: By experiment  
 OTHER INFORMATION: The promoter plus leader are responsible  
 OTHER INFORMATION: for expression of the bkd operon in *Pseudomonas putida*

FEATURE:  
 NAME/KEY: bkdA1, Gene encoding branched-chain keto acid  
 NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.  
 LOCATION: 805-2031. Initiating methionine codon is at  
 LOCATION: position 802, however mature peptide does not contain N-  
 LOCATION: terminal methionine.  
 IDENTIFICATION METHOD: By experiment  
 OTHER INFORMATION: The E1 component of branched chain keto  
 OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation  
 OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunits,  
 OTHER INFORMATION: E1 alpha and E1 beta.

FEATURE:  
 NAME/KEY: bkdA2, Gene encoding branched-chain keto acid  
 NAME/KEY: dehydrogenase-decarboxylase E1 beta subunit.  
 LOCATION: 2078-3091. Initiating methionine codon is position  
 LOCATION: 2075, however mature peptide does not contain N-terminal  
 LOCATION: methionine.  
 IDENTIFICATION METHOD: By experiment  
 OTHER INFORMATION: See description for Feature 2 above.

FEATURE:  
 NAME/KEY: bkdB, Gene encoding the E2 component of branched  
 NAME/KEY: chain keto acid dehydrogenase  
 LOCATION: 3098-4363 Initiating methionine codon is position  
 LOCATION: 3095, however mature peptide does not contain N-terminal  
 LOCATION: methionine.  
 IDENTIFICATION METHOD: By experiment  
 OTHER INFORMATION: E2 catalyzes the transacylation of the  
 OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzyme  
 OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3  
 OTHER INFORMATION: components.

FEATURE:  
 NAME/KEY: lpdV, Gene encoding the E3 component of branched  
 NAME/KEY: chain keto acid dehydrogenase.  
 LOCATION: 4369-5745. N-terminal methionine is present on  
 LOCATION: mature peptide.  
 IDENTIFICATION METHOD: By experiment  
 OTHER INFORMATION: E3 is lpd-val, the specific lipamide  
 OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the  
 OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched chain  
 OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.

PUBLICATION INFORMATION:  
 AUTHORS: Sokatch, John R.  
 AUTHORS: McCully, Vicki  
 AUTHORS: Gedrosky, Janet  
 AUTHORS: Sokatch, David, J.  
 TITLE: Isolation of a specific lipamide dehydrogenase  
 TITLE: for a branched-chain keto acid dehydrogenase  
 TITLE: from *Pseudomonas putida*  
 JOURNAL: Journal of Bacteriology  
 VOLUME: 148  
 ISSUE:  
 PAGES: 639-646  
 DATE: 1981  
 AUTHORS: Sokatch, John R.  
 AUTHORS: McCully, Vicki  
 AUTHORS: Roberts, C.M.  
 TITLE: Purification of a branched-chain keto acid  
 TITLE: dehydrogenase from *Pseudomonas putida*  
 JOURNAL: Journal of Bacteriology  
 VOLUME: 148  
 ISSUE:  
 PAGES: 647-652  
 DATE: 1981  
 AUTHORS: Sykes, Pamela  
 AUTHORS: Burns, Gayle  
 AUTHORS: Menard, Joan  
 AUTHORS: Hatter, Kenneth  
 AUTHORS: Sokatch, John R.  
 TITLE: Molecular cloning of genes encoding branched-chain  
 TITLE: keto acid dehydrogenase of *Pseudomonas putida*

JOURNAL: Journal of Bacteriology  
 VOLUME: 169  
 ISSUE:  
 PAGES: 1619-1625  
 DATE: 1987  
 AUTHORS: Burns, Gayle  
 AUTHORS: Brown, Tracy  
 AUTHORS: Hatter, Kenneth  
 AUTHORS: Sokatch, John R.  
 TITLE: Comparison of the amino acid sequences of the  
 TITLE: transacylase components of branched-chain oxoacid  
 TITLE: dehydrogenase of *Pseudomonas putida*, and the pyruvate and 2-  
 TITLE: oxoglutarate dehydrogenases of *Escherichia coli*  
 JOURNAL: European Journal of Biochemistry  
 VOLUME: 176  
 ISSUE:  
 PAGES: 165-169  
 DATE: 1988  
 AUTHORS: Burns, Gayle  
 AUTHORS: Brown, Tracy  
 AUTHORS: Hatter, Kenneth  
 AUTHORS: Idriess, John M.  
 AUTHORS: Sokatch, John R.  
 TITLE: Similarity of the E1 subunits of branched-chain-  
 TITLE: oxoacid dehydrogenase from *Pseudomonas putida* to the  
 TITLE: corresponding subunits of mammalian branched-chain-oxoacid  
 TITLE: and pyruvate dehydrogenases  
 JOURNAL: European Journal of Biochemistry  
 VOLUME: 176  
 ISSUE:  
 PAGES: 311-317  
 DATE: 1988  
 AUTHORS: Burns, Gayle  
 AUTHORS: Brown, Tracy  
 AUTHORS: Hatter, Kenneth  
 AUTHORS: Sokatch, John R.  
 TITLE: Sequence analysis of the lpdV gene for lipamide  
 TITLE: dehydrogenase of *Pseudomonas putida*  
 JOURNAL: European Journal of Biochemistry  
 VOLUME: 179  
 ISSUE:  
 PAGES: 61-69  
 DATE: 1989  
 AUTHORS: Madhusudan, K.T.  
 AUTHORS: Huang, G.  
 AUTHORS: Burns, Gayle  
 AUTHORS: Sokatch, J.R.  
 TITLE: Transcriptional analysis of the promoter region of  
 TITLE: the branched chain keto acid dehydrogenase operon of  
 TITLE: *Pseudomonas putida*  
 JOURNAL: Journal of Bacteriology  
 VOLUME: 172  
 ISSUE: October, 1990

Query Match 79.0%; Score 15.8; DB 1; Length 6122;  
 Best Local Similarity 89.5%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCATCATATTGCGCAGC 20  
 Db 4258 GTTCATCATCTTGCGCAGC 4240

RESULT 14  
 US-08-404-381-1/C  
 Sequence 1, Application US/08404381  
 Patent No. 6168945  
 GENERAL INFORMATION:  
 APPLICANT: Sokatch, John R.  
 APPLICANT: Sykes, Pamela Joy  
 APPLICANT: Madhusudan, K.T.  
 TITLE OF INVENTION: Genes Encoding Operon and Promoter for

TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of *Pseudomonas putida*  
TITLE OF INVENTION: and Methods  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carolyn D. Moon  
ADDRESS: Dunlap, Coddling, Peterson and Lee  
STREET: 9400 N. Broadway, Suite 420  
CITY: Oklahoma City  
STATE: Oklahoma  
COUNTRY: USA  
ZIP: 73114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 5.25 inch, 360 Kb Storage  
COMPUTER: IBM AT  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Professional Write 2.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/404,381  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,781  
FILING DATE:  
APPLICATION NUMBER: 07/172,148  
FILING DATE: 23-003-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Carolyn D. Moon  
REGISTRATION NUMBER: 33,022  
REFERENCE/DOCKET NUMBER: 5820.101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: Attorney, (405) 478-5344  
TELEFAX: Attorney, (405) 478-5349  
TELEX:  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6122 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Double stranded  
TOPOLOGY: Circular  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: Seq ID No. 61689451 is genomic DNA from *P. putida*  
DESCRIPTION: Strain PpG2 which contains the control region regulating  
DESCRIPTION: expression of the bkd operon and the four structural genes  
DESCRIPTION: of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No. 6168945 applicable  
ORIGINAL SOURCE:  
ORGANISM: *Pseudomonas putida*  
STRAIN: PpG2  
INDIVIDUAL ISOLATE: No. 6168945 applicable  
DEVELOPMENTAL STAGE: No. 6168945 applicable  
HARVOTYPE: No. 6168945 applicable  
TISSUE TYPE: No. 6168945 applicable  
CELL TYPE: Gram negative, aerobic Bactilli  
CELL LINE: No. 6168945 applicable  
ORGANELLE: No. 6168945 applicable  
IMMEDIATE SOURCE:  
LIBRARY: Genomic DNA from *Pseudomonas putida*  
CLONE: pURS54  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION: 35 Minutes  
UNITS:  
FEATURE:  
NAME/KEY: Promoter plus leader  
LOCATION: 1-792  
IDENTIFICATION METHOD: By experiment  
OTHER INFORMATION: The promoter plus leader are responsible  
OTHER INFORMATION: for expression of the bkd operon in *Pseudomonas putida*  
FEATURE:  
NAME/KEY: bkdA1, Gene encoding branched-chain keto acid  
NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.

LOCATION: 805-2031. Initiating methionine codon is at  
LOCATION: position 802, however mature peptide does not contain N-  
LOCATION: terminal methionine.  
IDENTIFICATION METHOD: By experiment  
OTHER INFORMATION: The E1 component of branched chain keto  
OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation  
OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunits,  
OTHER INFORMATION: E1 alpha and E1 beta.  
FEATURE:  
NAME/KEY: bkdA2, Gene encoding branched-chain keto acid  
NAME/KEY: dehydrogenase-decarboxylase E1 beta subunit.  
LOCATION: 2078-3091. Initiating methionine codon is position  
LOCATION: 2075, however mature peptide does not contain N-terminal  
LOCATION: methionine.  
IDENTIFICATION METHOD: By experiment  
OTHER INFORMATION: See description for Feature 2 above.  
FEATURE:  
NAME/KEY: bkdB Gene encoding the E2 component of branched  
NAME/KEY: chain keto acid dehydrogenase  
LOCATION: 3098-4363 Initiating methionine codon is position  
LOCATION: 3095, however mature peptide does not contain N-terminal  
LOCATION: methionine.  
IDENTIFICATION METHOD: By experiment  
OTHER INFORMATION: E2 catalyzes the transacylation of the  
OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzyme  
OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3  
OTHER INFORMATION: components.  
FEATURE:  
NAME/KEY: lpdV, Gene encoding the E3 component of branched  
NAME/KEY: chain keto acid dehydrogenase.  
LOCATION: 4369-5745. N-terminal methionine is present on  
LOCATION: mature peptide.  
IDENTIFICATION METHOD: By experiment  
OTHER INFORMATION: E3 is lpd-val, the specific lipamide  
OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the  
OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched chain  
OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.  
PUBLICATION INFORMATION:  
AUTHORS: Sokatch, John R.  
AUTHORS: McCully, Vicki  
AUTHORS: Gebrosky, Janet  
AUTHORS: Sokatch, David, J.  
TITLE: Isolation of a specific lipamide dehydrogenase  
TITLE: for a branched-chain keto acid dehydrogenase  
JOURNAL: Journal of Bacteriology  
VOLUME: 148  
ISSUE:  
PAGES: 639-646  
DATE: 1981  
AUTHORS: Sokatch, John R.  
AUTHORS: McCully, Vicki  
AUTHORS: Roberts, C.M.  
TITLE: Purification of a branched-chain keto acid  
TITLE: dehydrogenase from *Pseudomonas putida*  
JOURNAL: Journal of Bacteriology  
VOLUME: 148  
ISSUE:  
PAGES: 647-652  
DATE: 1981  
AUTHORS: Sykes, Pamela  
AUTHORS: Burns, Gayle  
AUTHORS: Menard, Joan  
AUTHORS: Hatter, Kenneth  
AUTHORS: Sokatch, John R.  
TITLE: Molecular cloning of genes encoding branched-chain  
TITLE: keto acid dehydrogenase of *Pseudomonas putida*  
JOURNAL: Journal of Bacteriology  
VOLUME: 169  
ISSUE:  
PAGES: 1619-1625  
DATE: 1987  
AUTHORS: Burns, Gayle

```

AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
TITLE: Comparison of the amino acid sequences of the
AUTHORS: Sokatch, John R.
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and 2-
TITLE: oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 165-169
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Idrees, John M.
AUTHORS: Sokatch, John R.
TITLE: Similarity of the E1 subunits of branched-chain-
TITLE: oxoacid dehydrogenase from Pseudomonas putida to the
TITLE: corresponding subunits of mammalian branched-chain-oxoacid
TITLE: and pyruvate dehydrogenases
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 311-317
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Sequence analysis of the lpdY gene for lipamide
Patent No. 6168945
TITLE: dehydrogenase of Pseudomonas putida
JOURNAL: European Journal of Biochemistry
VOLUME: 179
ISSUE:
PAGES: 61-69
DATE: 1989
AUTHORS: Madhusudan, K.T.
AUTHORS: Huang, G.
AUTHORS: Burns, Gayle
AUTHORS: Sokatch, J.R.
TITLE: Transcriptional analysis of the promoter region of
TITLE: the branched chain keto acid dehydrogenase operon of
TITLE: Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 172
Query Match          79.0%; Score 15.8; DB 3; Length 6122;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY      2 GTCCATCATATTGCGCAGC 20
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Db       4258 GTTCATCATCTTGCACGC 4240
RESULT 15
US-09-134-000C-2052/c
Sequence 2052, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2052

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; LENGTH: 582
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2052

Query Match          76.0%; Score 15.2; DB 4; Length 582;
Best Local Similarity 85.0%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGTCCATCATATTGCGCACG 20
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DB       218 TGTTCCTCATTTGCCACG 199

Search completed: April 1, 2004, 13:06:31
Job time : 43.5128 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:48:52 ; Search time 146.667 Seconds  
(without alignments)  
509.962 Million cell updates/sec

Title: US-09-520-538-17

Perfect score: 20  
Sequence: 1 tggccatcatattgacgacg 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2465228 seqs, 1869859620 residues

Total number of hits satisfying chosen parameters: 4930456

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications NA.\*

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2: /cgn2_6/prodata/2/pubpna/PCR_NEW_PUB.seq:*
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8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
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15: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-09-520-538-17	Sequence 17, Appl
2	16.4	82.0	1011	US-10-238-075-1134	Sequence 1134, Ap
3	16.4	82.0	1512	US-10-282-122A-17907	Sequence 17907, A
4	16.4	82.0	1770	US-10-133-403B-1	Sequence 1, Appl1
5	16.4	82.0	2768	US-09-380-773-1	Sequence 1, Appl1
6	16.4	82.0	41828	US-10-238-075-1117	Sequence 1117, Ap
7	16.4	82.0	48012	US-10-085-959-551	Sequence 251, App
8	16	80.0	363	US-09-864-408A-903	Sequence 903, App
9	15.8	79.0	215	US-10-424-599-95630	Sequence 95630, A
10	15.8	79.0	296	US-09-960-352-781	Sequence 781, App
11	15.8	79.0	441	US-10-282-122A-20650	Sequence 20650, A
12	15.8	79.0	562	US-10-424-599-120132	Sequence 120132, A
13	15.8	79.0	1269	US-10-282-122A-31336	Sequence 31336, A
14	15.8	79.0	1287	US-09-815-242-7768	Sequence 7768, Ap
15	15.8	79.0	1287	US-10-282-122A-30181	Sequence 30181, A

C 16	15.8	79.0	1715	12	US-10-424-599-55159	Sequence 55159, A
C 17	15.8	79.0	1806	12	US-10-425-114-1679	Sequence 1679, Ap
C 18	15.8	79.0	1824	9	US-09-938-842A-97	Sequence 97, Appl
C 19	15.8	79.0	1824	11	US-09-938-842A-97	Sequence 28366, A
C 20	15.8	79.0	2054	12	US-10-425-114-28366	Sequence 161, App
C 21	15.8	79.0	2936	14	US-10-114-170-161	Sequence 41643, A
C 22	15.4	77.0	362	12	US-10-424-599-41643	Sequence 31, Appl
C 23	15.4	77.0	2363	14	US-10-272-665-31	Sequence 31, Appl
C 24	15.4	77.0	2363	14	US-10-272-665-31	Sequence 31, Appl
C 25	15.4	77.0	2363	14	US-10-273-321-31	Sequence 31, Appl
C 26	15.4	77.0	2363	14	US-10-272-756-31	Sequence 31, Appl
C 27	15.4	77.0	2363	14	US-10-272-756-31	Sequence 31, Appl
C 28	15.4	77.0	2363	14	US-10-273-228-31	Sequence 31, Appl
C 29	15.4	77.0	2363	15	US-10-273-228-31	Sequence 31, Appl
C 30	15.4	77.0	2363	15	US-10-273-228-31	Sequence 31, Appl
C 31	15.4	77.0	2363	15	US-10-428-254A-63	Sequence 63, Appl
C 32	15.2	76.0	215	9	US-09-960-352-781	Sequence 1411, Ap
C 33	15.2	76.0	446	10	US-09-918-995-26516	Sequence 26516, A
C 34	15.2	76.0	860	15	US-10-027-632-137631	Sequence 137631, A
C 35	15.2	76.0	862	15	US-10-027-632-137631	Sequence 137631, A
C 36	15.2	76.0	882	15	US-10-282-122A-40282	Sequence 40282, A
C 37	15.2	76.0	923	15	US-10-398-221-1423	Sequence 1423, Ap
C 38	15.2	76.0	1365	9	US-09-738-626-3027	Sequence 3027, Ap
C 39	15.2	76.0	1836	15	US-10-369-493-37526	Sequence 37526, A
C 40	15.2	76.0	1880	12	US-10-424-599-1505	Sequence 1505, Ap
C 41	15.2	76.0	1908	12	US-10-425-114-11437	Sequence 11437, A
C 42	15.2	76.0	1933	12	US-10-428-599-1507	Sequence 1507, Ap
C 43	15.2	76.0	2433	15	US-10-369-493-47329	Sequence 47329, A
C 44	15.2	76.0	3325	12	US-10-425-114-30682	Sequence 30682, A
C 45	15.2	76.0	3432	12	US-10-282-122A-29275	Sequence 29275, A

## ALIGNMENTS

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RESULT 1
US-09-520-538-17
Sequence 17, Application US/09520538
Patent No. US20020168636A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Wise, Ariene
TITLE OR INVENTION: Detection Of Phenols Using Engineered Bacteria
FILE REFERENCE: S-91.714
CURRENT APPLICATION NUMBER: US/09/520.538
CURRENT FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 20
TYPE: DNA
ORGANISM: Pseudomonas sp. CF600
US-09-520-538-17
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Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 TGTCCATCATATTGCGACG 20
Db 1 TGTCCATCATATTGCGACG 20

RESULT 2
US-10-238-075-1134/c
Sequence 1134, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolated from a source of polynucleotides and of these polynucleotides and of the
FILE REFERENCE: Blandine
CURRENT APPLICATION NUMBER: US/10/238.075
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CURRENT FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: 0003145  
PRIOR FILING DATE: 2000-03-10  
NUMBER OF SEQ ID NOS: 1576  
SOFTWARE: Patent version 3.1  
SEQ ID NO 1134  
LENGTH: 1011  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-10-238-075-1134

Query Match 82.0%; Score 16.4; DB 14; Length 1011;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTTCATCATATTGGCGCA 18  
DB 197 TGTTCATCATATTGGCGCA 180

RESULT 3  
US-10-282-122A-17907/c  
Sequence 17907, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: Patent version 3.1  
SEQ ID NO 17907  
LENGTH: 1512  
TYPE: DNA  
ORGANISM: Corynebacterium diphtheriae  
US-10-282-122A-17907

Query Match 82.0%; Score 16.4; DB 12; Length 1512;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 1206 TCCATCATATTGGCGACG 1189

RESULT 4  
US-10-133-403B-1/c  
Sequence 1, Application US/10133403B  
Publication No. US20030096115A1  
GENERAL INFORMATION:  
APPLICANT: Shinya Kozaki, Tetsuya Yano, Teiyoshi No. US20030096115A1, Tsutomu Hom  
TITLE OF INVENTION: Granular Structure and Process of Production Thereof  
FILE REFERENCE: 03500.016384  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: US/10/133,403B  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Microsoft Word  
SEQ ID NO 1  
LENGTH: 1770  
TYPE: DNA  
ORGANISM: Ralstonia eutropha TB64  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1770) PolymyxinDutyrate synthase encoding sequence  
US-10-133-403B-1

Query Match 82.0%; Score 16.4; DB 14; Length 1770;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 563 TCCATCATATTGGCGACG 546

RESULT 5  
US-09-380-773-1/c  
Sequence 1, Application US/09380773  
Publication No. US20030113884A1  
GENERAL INFORMATION:  
APPLICANT: Hein, Silke  
APPLICANT: Soling, Brigitte  
APPLICANT: Gotschalk, Gerhard  
APPLICANT: Steinbuechel, Alexander  
TITLE OF INVENTION: Methods for the Biosynthesis of Polyesters  
FILE REFERENCE: NOB1136---11899.0136.NPUS00  
CURRENT APPLICATION NUMBER: US/09/380,773  
CURRENT FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: PCT/US97/03994  
PRIOR FILING DATE: 1997-03-03  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent version 3.0  
SEQ ID NO 1  
LENGTH: 2768  
TYPE: DNA  
ORGANISM: Ralstonia eutropha  
US-09-380-773-1

Query Match 82.0%; Score 16.4; DB 10; Length 2768;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATCATATTGGCGACG 20  
DB 1404 TCCATCATATTGGCGACG 1387

RESULT 6  
US-10-238-075-1117/c  
Sequence 1117, Application US/10238075

```

Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANT: I.N.S.B.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1117
LENGTH: 41828
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12048)..(12048)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17019)..(17020)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17023)..(17026)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17030)..(17030)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21033)..(21033)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (29608)..(29611)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (32059)..(32059)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (32185)..(32185)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (35059)..(35059)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (35140)..(35140)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (35144)..(35144)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37006)..(37006)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37055)..(37055)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37058)..(37058)
OTHER INFORMATION: unknown
FEATURE:

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NAME/KEY: misc_feature
LOCATION: (37086)..(37086)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37391)..(37391)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40956)..(40956)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41367)..(41367)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41375)..(41375)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41380)..(41380)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41382)..(41382)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41384)..(41384)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41723)..(41723)
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41771)..(41771)
OTHER INFORMATION: unknown
US-10-238-075-1117

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```

Query Match      82.0%; Score 16.4; DB 14; Length 41828;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 TGTCCATCATATTGGCGCA 18
Db      25139 TGTCCATCAATTGGCGCA 25122

```

```

RESULT 7
US-10-085-959-251/C
; Sequence 251, Application US/10085959
; Publication No. US20030165870A1
GENERAL INFORMATION:
APPLICANT: Welch, Rodney A.
APPLICANT: Bland, Valerie D.
TITLE OF INVENTION: No. US20030165870A1 Sequence of E. Coli CFT073
FILE REFERENCE: 960296, 97648
CURRENT APPLICATION NUMBER: US/10/085,959
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/242,412
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 255
SOFTWARE: PatentIn version 3.1
SEQ ID NO 251
LENGTH: 48012
TYPE: DNA

```



```

ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (12004)..(20508)
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: (40330)..(44949)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (13480)..(13480)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (31038)..(31038)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (31042)..(31042)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (31770)..(31770)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (31799)..(31799)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (44922)..(44922)
OTHER INFORMATION: Unsure
US-10-085-959-251

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```

Query Match      82.0%; Score 16.4; DB 14; Length 48012;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TGTCCATCATATTGGCGCA 18
DB 3562 TGTCCATCATATTGGCGCA 3545

```

```

RESULT 8
US-09-864-408A-903/c
Sequence 903, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: leach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enc
FILE REFERENCE: 21402-02
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 903
LENGTH: 363
TYPE: DNA
ORGANISM: Homo sapiens
US-09-864-408A-903

```

```

Query Match      80.0%; Score 16; DB 11; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 TCCATCATATTGGCGCA 18
DB 132 TCCATCATATTGGCGCA 117

```

```

RESULT 9
US-10-424-599-95630
Sequence 95630, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J.

```

```

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 95630
LENGTH: 215
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_57365C.1
US-10-424-599-95630

```

```

Query Match      79.0%; Score 15.8; DB 12; Length 215;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 TGTCCATCATATTGGCGCAC 19
DB 168 TGTCCATCATATTGGCGCAC 186

```

```

RESULT 10
US-09-960-352-781
Sequence 781, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathiasagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 781
LENGTH: 296
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 04-LIB3057-008-Q1-K1-A7
US-09-960-352-781

```

```

Query Match      79.0%; Score 15.8; DB 9; Length 296;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 GTCCATCATATTGGCGCAG 20
DB 65 GTCCATCATATTGGCGCAG 83

```

```

RESULT 11
US-10-282-122A-20650/c
Sequence 20650, Application US/10282122A
Publication No. US20040029125A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

```

APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20650  
LENGTH: 441  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-10-282-122A-20650

Query Match 79.0%; Score 15.8; DB 12; Length 441;  
Best Local Similarity 89.5%; Pred. No. 2.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTCATCATATTGGCAGC 19  
DB 436 GTTCATCATCTTGGCAGC 418

RESULT 12  
US-10-424-599-120132/c  
Sequence 120132, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 120132  
LENGTH: 562  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_79487C.1  
US-10-424-599-120132

Query Match 79.0%; Score 15.8; DB 12; Length 562;  
Best Local Similarity 89.5%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTCATCATATTGGCAGC 19  
DB 291 GTTCATCATATTGGCAGC 273

RESULT 13  
US-10-282-122A-31336/c  
Sequence 31336, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31336  
LENGTH: 1269  
TYPE: DNA  
ORGANISM: Pseudomonas putida  
US-10-282-122A-31336

Query Match 79.0%; Score 15.8; DB 12; Length 1269;  
Best Local Similarity 89.5%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GTTCATCATATTGGCAGC 20  
DB 1164 GTTCATCATCTTGGCAGC 1146

RESULT 14  
US-09-815-242-7768/c  
Sequence 7768, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant U.  
APPLICANT: Yamamoto, Robert T.

```

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 7768
LENGTH: 1287
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1287)
US-09-815-242-7768

```

```

Query Match          79.0%; Score 15.8; DB 9; Length 1287;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2  GTCCATCATTTGGCGACG 20
DB      1179 GTTCATCATCTTGGCGACG 1161

```

```

RESULT 15
US-10-282-122A-30181/C
Sequence 30181, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23

```

```

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 30181
LENGTH: 1287
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30181

```

```

Query Match          79.0%; Score 15.8; DB 12; Length 1287;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2  GTCCATCATTTGGCGACG 20
DB      1179 GTTCATCATCTTGGCGACG 1161

```

```

Search completed: April 1, 2004, 13:13:34
Job time : 147.667 secs

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